

IN THE CLAIMS:

The text of all pending claims, (including withdrawn claims) is set forth below. Cancelled and not entered claims are indicated with claim number and status only. The claims as listed below show added text with underlining and deleted text with ~~strikethrough~~. The status of each claim is indicated with one of (original), (currently amended), (cancelled), (withdrawn), (new), (previously presented), or (not entered).

Please AMEND claims 16, 17, 23, 24 and 25 and ADD new claim 26 in accordance with the following:

1-15. (Cancelled)

16. (Currently Amended) A method of determining spatially similar portions of substances by analyzing three-dimensional structures of the substances including a first structure expressed by three-dimensional coordinates of elements belonging to a first point set of an amino acid sequence database or a motif database and a second structure expressed by three-dimensional coordinates of elements belonging to a second point set of an input amino acid sequence~~and automatically determine a distance between the elements of the first point set and the elements of the second point set that have an optimal correspondence~~, comprising:

dividing the first point set and second point set into first subsets and second subsets, respectively, according to a secondary structure exhibited by the three-dimensional coordinates of the elements of the first and the second point sets;

generating a combination of correspondence satisfying a first restriction condition between the first subsets and the second subsets from among candidates for the combination of correspondence;

determining the optimum correspondence between the elements belonging to each pair of subsets corresponding in the combination of correspondence generated; and

calculating a root mean square distance between all of the elements corresponding in the optimum correspondence to automatically determine a distance between the elements of the first point set and the elements of the second point set that have an optimal correspondence and to determine a length of a longest common subsequence (LCS) between a character sequence expressing the input amino acid sequence and a character sequence expressing the amino acid sequence having a greatest correspondence to the input amino acid sequence.

17. (Currently Amended) The method of claim 16, wherein determining the optimum correspondence comprises:

generating a combination of correspondence satisfying a second restriction condition between the elements belonging to the subsets corresponding in the combination of the correspondence generated;

calculating a root mean square distance between the elements corresponding in the combination of the correspondence generated satisfying the second restriction condition; and

selecting a combination of the correspondence as the optimum correspondence according to the value of the root mean square distance value calculated to determine the LCS and an occurrence position of the LCS between the character sequence expressing the input amino acid sequence and the character sequence having the greatest correspondence and expressing an amino acid sequence taken from the amino acid sequence database or the motif database and align the character sequence of the input amino acid sequence with the character sequence having the greatest correspondence and expressing the amino acid sequence from the amino acid sequence database or the motif database, based on the LCS and the occurrence position of the LCS, by inserting a blank corresponding to a length of a character sequence between positions of subsequences.

18-22. (Cancelled)

23. (Currently Amended) An apparatus for determining spatially similar portions of substances by analyzing three-dimensional structures of the substances including a first structure expressed by three-dimensional coordinates of elements belonging to a first point set of an amino acid sequence database or a motif database and a second structure expressed by three-dimensional coordinates of elements belonging to a second point set of an input amino acid sequence and automatically determining a distance between the elements of the first point set and the elements of the second point set that have an optimal correspondence, comprising:

a dividing unit to divide the first point set and the second point set into first subsets and second subsets, respectively, according to a secondary structure exhibited by the three-dimensional coordinates of the elements of the first and the second point sets;

a generating unit to generate a combination of correspondence satisfying a first restriction condition between the first subsets and the second subsets from among candidates for the combination of correspondence;

a determining unit to determine an optimum correspondence between the elements belonging to each pair of subsets corresponding in the combination of correspondence generated in the generating unit, and

a calculating unit to calculate a root mean square distance between all of the elements corresponding in the optimum correspondence, to automatically determine a distance between

the elements of the first point set and the elements of the second point set that have an optimal correspondence and to determine a length of a longest common subsequence (LCS) between a character sequence expressing the input amino acid sequence and a character sequence expressing the amino acid sequence having a greatest correspondence to the input amino acid sequence.

24. (Currently Amended) A computer-readable medium containing computer-readable instructions to determine spatially similar portions of substances by analyzing three-dimensional structures of the substances including a first structure expressed by three-dimensional coordinates of elements belonging to a first point set of an amino acid sequence database or a motif database and a second structure expressed by three-dimensional coordinates of elements belonging to a second point set of an input amino acid sequence and automatically determining a distance between the elements of the first point set and the elements of the second point set that have an optimal correspondence, the computer-readable instructions comprising:

dividing the first point set expressing a position of an amino acid of the amino acid sequence taken from the amino acid sequence database or the motif database and second point set expressing a position of an amino acid of the input amino acid sequence into first subsets and second subsets, respectively, according to a secondary structure exhibited by the three-dimensional coordinates of the elements of the first and the second point sets;

generating a combination of correspondence satisfying a first restriction condition between the first subsets and the second subsets from among candidates for the combination of correspondence;

determining the optimum correspondence between the elements belonging to each pair of subsets corresponding in the combination of correspondence generated; and

calculating a root mean square distance between all of the elements corresponding in the optimum correspondence, automatically determining a distance between the elements of the first point set and the elements of the second point set that have an optimal correspondence and and determining a length of a longest common subsequence (LCS) between a character sequence expressing the input amino acid sequence and a character sequence expressing the amino acid sequence having a greatest correspondence to the input amino acid sequence.

25. (Previously Presented) The computer-readable medium of claim 24, wherein determining the optimum correspondence comprises:

generating a combination of correspondence satisfying a second restriction condition between the elements belonging to the subsets corresponding in the combination of the

correspondence generated; calculating a root mean square distance between the elements corresponding in the combination of the correspondence generated satisfying the second restriction condition; and selecting a combination of the correspondence as the optimum correspondence according to the value of the root mean square distance value calculated, determining the LCS and an occurrence position of the LCS between the character sequence expressing the input amino acid sequence and the character sequence having the greatest correspondence and expressing an amino acid sequence taken from the amino acid sequence database or the motif database, and aligning the character sequence of the input amino acid sequence with the character sequence having the greatest correspondence and expressing the amino acid sequence from the amino acid sequence database or the motif database, based on the LCS and the occurrence position of the LCS, by inserting a blank corresponding to a length of a character sequence between positions of subsequences.

26. (New) A computer-readable medium containing computer-readable instructions to compare spatially similar portions of an input amino acid sequence and an amino acid sequence taken from an amino acid sequence database or a motif database, the computer-readable instructions comprising:

searching the amino acid sequence database and the motif database for an amino acid sequence or sequences having at least a predetermined degree of similarity to the input amino acid sequence;

determining a length of a longest common subsequence (LCS) between a character sequence expressing the input amino acid sequence and a character sequence expressing the amino acid sequence having a greatest degree of similarity to the input amino acid sequence, wherein the amino acid sequence having the greatest degree of similarity is selected from a set of amino acid sequences having at least the predetermined degree of similarity;

determining the LCS and an occurrence position of the LCS between the character sequence expressing the input amino acid sequence and the character sequence having the greatest degree of similarity and expressing an amino acid sequence taken from the amino acid sequence database or the motif database; and

aligning the character sequence of the input amino acid sequence with the character sequence having the greatest degree of similarity and expressing the amino acid sequence from the amino acid sequence database or the motif database, based on the LCS and the occurrence position of the LCS, by inserting a blank corresponding to a length of a character sequence between positions of subsequences.